IN THE CLAIMS:

Please amend the claims as follows:

1. (Currently Amended) A method for identifying the presence of a bacterium in a sample comprising

a) testing said sample by Gram-staining and determining the rod or coccus character of said bacterium and when said Gram-staining indicates the presence of a Gram-positive bacterium with a coccus character, further determining a chain-like or clump-like character of said bacterium,

b) testing said sample with a probe according to an *in situ* hybridisation protocol selected on the basis of the outcome of said Gram-staining, said method further comprising

(i) when said Gram-staining indicates the presence of a Gram-negative bacterium with a coccus character, subjecting said sample to a treatment with a lysis buffer comprising lysozyme, and

(ii) when said Gram-staining indicates the presence of a Gram-positive bacterium with a rod character, subjecting said sample to a treatment with a lysis buffer comprising lysozyme and/or Proteinase K, and

(iii) when said Gram-staining indicates the presence of a Gram-positive bacterium with a coccus and chain-like character subjecting said sample to a treatment with a lysis buffer comprising lysozyme and,

(iv) when said Gram-staining indicates the presence of a Gram-positive bacterium with a coccus and clump-like character subjecting said sample to a treatment with a lysis buffer comprising lysostaphin ~~and~~/or Proteinase K or a combination thereof,

and identifying the presence of the bacterium in the sample.

2. (Previously Presented) A method according to claim 1 wherein said sample is a clinical sample.

3. (Previously Presented) A method according to claim 2 wherein said sample is mammalian blood.

4. (Canceled)

5. (Currently Amended) A method according to claim 1 wherein said character is of the Gram-negative rod type, further comprising hybridising said sample with at least one probe selected from athe group of probes for detecting nucleic acid found in an organism selected from the group consisting of *Escherichia coli*, *Klebsiella pneumoniae*, *Klebsiella oxytoca*, *Serratia marcescens*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Proteus vulgaris*, *Proteus mirabilis*, *Salmonella typhi*, and

Pseudomonas aeruginosa.

6. (Previously Presented) A method according to claim 5 wherein said nucleic acid is ribosomal RNA.

7. (Previously Presented) A method according to claim 6 wherein said probe is selected from the group consisting of

GCCTGCCAGTTTCGAATG (SEQ ID NO:1)or

GTAGCCCTACTCGTAAGG (SEQ ID NO:2) or

GAGCAAAGGTATTAACTTTACTCCC (SEQ ID NO:3) or

GTTAGCCGTCCCTTTCTGG (SEQ ID NO:4).

8-12 (Canceled)

13. (Currently Amended) A method according to claim 1, wherein said character is of a Gram-positive chain-like coccus type further comprising hybridising said sample with at least one probe selected from ~~a~~the group consisting of probes for detecting nucleic acid found in an organism selected from the group consisting of *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Streptococcus mitis*, *Streptococcus viridans*, *Streptococcus sanguis*, and *Enterococcus faecium*.

14. (Previously Presented) A method according to claim 13 wherein said nucleic acid is ribosomal RNA.

15. (Previously Presented) A method according to claim 14 wherein said probe is selected from the group consisting of TTATCCCCCTCTGATGGG (SEQ ID NO:5)or

AGAGAAGCAAGCTTCTCGTCCG (SEQ ID NO:6)or GCCACTCCTCTTTTTCCGG (SEQ ID NO:7).

16. (Canceled)

17. (Currently Amended) A method according to claim 1, wherein said character is of a Gram-positive clumb-like coccus type further comprising hybridising said sample with at least one probe selected from ~~a~~the group consisting of probes for detecting nucleic acid found in an organism selected from the group consisting of *Staphylococcus aureus*, *Staphylococcus haemolyticus*, and *Staphylococcus saprophyticus*.

18. (Previously Presented) A method according to claim 17 wherein said nucleic acid is ribosomal RNA.

19. (Previously Presented) A method according to claim 18 wherein said probe is selected from the group consisting of GCTAATGCAGCGCGGATCC (SEQ ID NO:8) or

CCGAAGGGGAAGGCTCTA (SEQ ID NO:9) or AGAGAAGCAAGCTTCTCGTCCGTT (SEQ ID NO:10).

20. (Currently Amended) A method according to claim 1 further comprising hybridising said sample

with at least one positive control probe ~~and/~~or with at least one negative control probe.

21. (Previously Presented) A method according to claim 20 wherein said positive control probe consists of the sequence GCTGCCTCCCGTAGGAGT (SEQ ID NO:11) and/or wherein said negative control probe of the sequence ACTCCTACGGGAGGCAGC (SEQ ID NO:12).

22. (Previously Presented) A method according to claim 1 further comprising a one-step procedure of binding bacteria present in said sample to a microscopic slide and simultaneously fixing intracellular structures.